## STIC-Biot ch/Ch mLib

68015

From:

Chan, Christina

Sent: To:

Subject:

Tuesday, June 04, 2002 1:46 PM Sorbello, Eleanor; STIC-Biotech/ChemLib RE: Rush seq search 09/515,369B

## Please rush. Thanks Chris

----Original Message----

From:

Sorbello, Eleanor

Sent:

Tuesday, June 04, 2002 1:28 PM

To: Cc: Chan, Christina Sorbello, Eleanor

Subject:

Rush seq search 09/515,369B

Christina.

Can you please reqest a rush seq. search of (1) nucleotide <u>SEQ. ID. NO: 1</u> and (2) any matches from T at position -2241 to the C at posn. 0 of Seq. ld NO: 1

Eleanor Sorbello, Art Unit 1632 / CM1 12D14 V (703) 308-6043

Numbering does not correspond to our database system

of membering.

In our files the first 10 positions are: taatacgact.

There is no zero position and there are no regative numbers.

Point of Contact: **Toby Port** Technical Info. Specialist CM1 6A04 703-308-3534

	TYPE OF SEARCH:	VENDOR/COST(where applic.)
Searcher:	NA Sequences:	STN:
Phone:	AA Sequences:	DIALOG:
Location:	Structures:	Questel/Orbit:
Date Picked Up: 6/3	Bibliographic:	DRLink:
Date Completed:	Litigation:	Lexis/Nexis:
Searcher Prep/Review:	Full text:	Sequence Sys.:
Clerical:	Patent Family:	WWW/Internet:
Online time:	Other:	Other (specify):

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2256)
Madireddi,M.T., Dent,P. and Fisher,P.B.
Madireddi,M.T., Dent,P. and Fisher,P.B.
Promoter activity during human melanoma differentiation
J. Cell. Physiol. 185 (1), 36-46 (2000)
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Madireddi,M.: and Fisher,P.B.
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AF275916

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AC108684

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Minimum DB seq Maximum DB seq

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Direct Submission
Submitted (06-NOV-2001) Genome Center, University of Washington,
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On Nov 6, 2001 this sequence version replaced gi:10277966.
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Quality coverage: 10.0x in Q20 bases; sum-of-contigs
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
1 (bases 1 to 193317)
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Sequencing vector: plasmid: L08752; 61% of reads
Chemistry: Dye-terminator ET; 89% of reads
Chemistry: Dye-terminator ET; 89% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 192768 bases at least Q40
Consensus quality: 193102 bases at least Q40
Consensus quality: 193102 bases at least Q20
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Contact: uwgchtgs@u.washington.edu
Drafting Center: SC
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Center project name: chr-1
Center clone name: RP11-564A8 (sc0742)
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Db 103494 GGCTCGATCACCTTTTGAACCCAGGTCTGCCTGCCTCCAAAGCTTGTACTCATAACTAGA 103553
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                      is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
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/db_xref="taxon:9606"
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/chromosome="la"
/clone="RP11-564A8"
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QQ Op	Oy Dp	Qy Db	Oy Db	Qy Db	O.y D.b	Oy Dp	Qy Dp	Oy Dp	Qy Dp	ço D	Oy Db	Qy Db	9 9	Oy Dp	Qy	Oy Db	Qy Db	δý

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Upublished

Stren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwith, J., Barnan, N., Beddar, F., Boguslavkiy, L., Baldwith, J., Barnan, N., Beddar, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campoplano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Dodge, S., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grand, G., Hagos, B., Haaford, A., Horton, L., Karatas, A., Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Lieu, C., Liu, G., Lock, K., MacConnal, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKarnan, K., McPheeters, R., Meidrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Mortow, J., Naylor, J., Peterson, K., Pierre, N., Pierre, N., Pierre, N., Pierre, N., Patana, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC023534 229302 bp DNA linear HTG 04-MAY-2000 HOMO sapiens clone RPll-462N18, WORKING DRAFT SEQUENCE, 41 unordered pieces.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 229302)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome, clone RP11-462N18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        2046 tcaaacccaggtctcatctcacctcagggggctgctttccccatcgctgtattgtccttaa
                                                                          gggcatcattattgaattattttgacaggaaggagactggtgtatgctgcacagtaataa
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AC023534.3 GI:7705140
HTG: HTGS_PHASE1; HTGS_DRAFT.
human.
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TITLE JOURNAL COMMENT

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97169 97268: 94p of 100 bp 1019059 1100 bp 101906: contig of 4638 bp in length 101907 102007 109439: contig of 4638 bp in length 102007 109439: contig of 7433 bp in length 109440 109539: 94p of 100 bp 10940 117593 117592: contig of 8053 bp in length 117593 117592: contig of 8053 bp in length 117593 117593: contig of 8053 bp in length 126038 125137: 94p of 100 bp 125138 135140: contig of 9003 bp in length 135141 135240: 94p of 100 bp 13541 146384: contig of 11144 bp in length 14688 146484: 94p of 100 bp 160353 166452: 94p of 1300 bp 160353 166452: 94p of 1300 bp 173458
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                                                                                                                                          162: gap of 100 bp 45898: contig of 3936 bp in length
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61336: contig of 5890 bp in length
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79878: contig of 4892 bp in length
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89873: contig of 5493 bp in length
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97168: contig of 7195 bp in length
                                         in length
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RPLI-462NL8"
/clone_lib="RPCI-11 Human Male
                                                        35050: gap of 100 bp
38193: contig of 3143 bp
38293: gap of 100 bp
41862: contig of 3569 bp
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                     34950: contig of 2355 bp
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50904: contig of 4906 bp
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/note="assembly_fragment"
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Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.
                                                                                                                                            Genome
                                                                                                                                                                                                                                                             Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                Direct Submission
Submitted (15-FBB-2000) Whitehead Institute/MIT Center for Submitted (15-FBB-2000) Whitehead Institute/MIT Center for May 4, 200 Charles Street, Cambridge, MA 02141, 05A.
On May 4, 2000 this sequence version replaced gi:7143452.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 41 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                  Conter clone name: 462_N.18

Sequencing vector: M13, M77815, 100% of reads
Sequencing vector: M13, M77815, 100% of reads
Chemistry: Dye-terminator B19 bye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 194690 bases at least 040
Consensus quality: 207622 bases at least 030
Consensus quality: 207622 bases at least 030
Consensus quality: 217061 bases at least 020
Insert size: 200000; agarose-fp
Insert size: 253002; sum-of-contigs
Quality coverage: 4.5 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                    Center code: WIBR
Web site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center project Information
Center project name: L5244
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of 1313 bp in length
100 bp
of 1198 bp in length
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1109 1208: gap of 100 bp
1250 2504: contig of 1296 bp in length
2505 2604: gap of 100 bp
2605 3688: contig of 1084 bp in length
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14467: contig of 1627 bp in length
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19176: contig of 2096 bp in length
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26561: contig of 2635 bp in length
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28846: contig of 2185 bp in length
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32495: contig of 3549 bp in length
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/673: contig of 1
17773: gap of 100
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23826: contig of
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6375: con
5: gap of
7673: con
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4962: con
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157296 157116 156876 156636 1104 1284 1823 924 aaccagacaggaactattttaggctctgtgtgccatatggtctcagtcacaactactcat CAGGGATTGCAAAGGAGTATTTGTTTGCTTAAGAAAATAAACAACACTGAGTATGAGAT tcactctcctctttctttcatctccactgagctggaggcagttatcctgtccccacgt ATGAAAACTITATITATTATGGATACGGAAACCTGAAAATAATGTCTTTTGATTTT ttocccaatcattaaaaaacgtaaaaactactattaggtcgcaaggttaagccattotca atgaaaactttatttattatggatacggaaacctgaaaataatgtcttcttttgatttt actageccaccagageaccaggecteceagetttetgggettgtecatgegtacatttee

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AC068122 180048 bp DNA linear HTG 07-JUL-2000 HOMO Sapiens chromosome 1 clone RP11-237C22, WORKING DRAFT SEQUENCE, 28 unordered pieces.
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Submitted (28-APR-2000) Genome Sequencing Center, Washington
Iniversity School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On May 18, 2000 this sequence version replaced 91:7717167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 180048)
Waterston, R. H.
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NOTE: This is a 'working draft' sequence. It currently consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                              Insert size: 167000; agarose-fp
Insert size: 177348; sum-of-contigs
Quality coverage: 3.90 in Q20 bases; agarose-fp
Quality coverage: 3.76 in Q20 bases; sum-of-contigs
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Consensus quality: 165826 bases at least Q20
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90 Pp	1522 82204	gacacatcacgctgtctgtgtcccctgagtggttcagagc 
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Homo sapiens interleukin 24 (IL24) gene, complete cds.
AY062931
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AUTHORS
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JOURNAL
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Query Match
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Matches 1916; Conservative
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1082
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5389
                                                                                                                                                        'gene-"IL24"
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ggtctcagtcacaactactcatctctgcctctgtagcacgaaagcaattagcaacaatat 1022
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                                                                                                                                                                                                                                                                       cctaaatccacatggtgggaagggggggggtgggggaagagaggtgcgctgtggggctgtgc 602
                                                                                                                                                         Gaps
                                                   81.9%; Score 1872.2; DB 9; Length 11114; 98.6%; Pred. No. 0;
                                                                 19;
                                                                 Indels
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TKALGEVDILLTWMQKFYKL"

1 others DNA linear PRI 20-DEC-2000 on association protein 7 gene, 3; of Surgery, University of Glasgow Royal Infirmary, Glasgow ntiation association protein 7" 80,4261. .4323,5460. .5618, ntiation association protein 7" ata; Vertebrata; Euteleostomi; rhini; Hominidae; Homo. 180,4261. .4323,5460. .5618, 1208 gccaatcoctgattcccaaaatgtattcctcagggatgtggggaaatacttatgggaagt 1267 14; Indels 22; Gaps ger, S. and Gallagher, G. ger, S. and Gallagher, G. DB 9; Length 7025; δ

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               361 GCCAATCCCTGATTCCCAAAATGTATTCCTCAGGGATGTGGGCAAATACTTATGGGAAAT 420
                                                                                                                                                   ttgtttttgcctttgtttattacactt-----
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Telkami, M., Kirsch, S., Schiller, S., Richter, A., Benes, V., Franco, B., Murcya, K., Rao, E., Merker, S., Niesler, B., Ballablo, A., Ansorge, W., Ogata, T. and Rappold, G.A.
A member of a gene family on xp22.3, VCX-A, is deleted in patients with X-linked nonspecific mental retardation
Am. J. Hum. Genet. 67 (3), 563-573 (2000)
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HSA243947 29034 bp DNA linear PRI 09-NOV-2000
Homo sapiens VCX-A gene for variably charged X chromosome protein.
AJ243947
                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 29034)
Lix.M., Yen.P. H. and Shapiro, L.J.
Characterization of a low copy repetitive element S232 involved in
the generation of frequent deletions of the distal short arm of the
                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (10-AUG-1999) Richter A., Biochemical Instrumentation,
EMBL, Meyerhofstrasse 1, Heidelberg, 69117, GERMANY
Location, Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_line="lymphoblastoid"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         human X chromosome
Nucleic Acids Res. 20 (5), 1117-1122 (1992)
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1 (bases 1 to 174210)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,

Alsbrooks, S.L., Amaratunge, H.C., Are, Y.R., Ayele, M., Banks, T.,

Barbaria, J., Benton, J., Bindge, K., Blankenburg, K., Bondin, D.,

Bouck, J., Bowde, S., Briteva, M., Brown, E., Brown, M., Bryant, N.P.,

Bunay, C., Burch, P., Burkett, C., Burcell, K.L., Byrd, N.C.

Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,

Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,

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Delaney, R.R., Deladoo, Denn, A.L., Ding, Y., Dinh, H.,

Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Punbin, K.J.,

Barnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,

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Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,

Hernandez, O., Hodgson, A., Hully, S., Hume, J., Jackson, L. B.,

Jacobson, B., Jla, Y., Johnson, R., Johlivet, S., Joudah, S.,

Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,

Kratovic, J., Kueseh, A., Lucier, Marbabat, K., Martin, R., Mattin, R., Pickens, R., Pic
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                               4261 TGAAGACAATATGGTCTCTTTTACAACTACTCATCTCTGCCTTTGTAGCAAAAAAACAGC 4320
                                                                                                                                                                                                                                                                                                                                                            891 ctggacccaggttgggcaaactcttcctgtaaagaaccagacaggaactatttaggctc 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens chromosome Xp clone RP11-359020, WORKING DRAFT SOUBNCE, 4 unordered pleces.
                                                                                                                                                                                                                                               4.0%; Score 91.8; DB 9; Length 29034; 75.5%; Pred. No. 1.7e-14;
Live 0; Mismatches 37; Indels 0;
                                                                                                                                       71 others
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AC108684/c
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Consensus quality: 171318 bases at least Q30
Consensus quality: 171608 bases at least Q20
Estimated insert size: 170099; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 9.9x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (31-7Am-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza; Houston, TX 77030, USA
Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Matlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, Y., Wu, Y. Y., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: Plasmid; M77789
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329First call to
findPhrapList
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Pred. No. 1.8e-14;
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76782: gap of unknown length
150776: contig of 73894 bp in length
150776: gap of unknown length
164461: contig of 13885 bp in length
16451: gap of unknown length
174210: contig of 9649 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Baylor College of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: HDOM
Center clone name: RP11-359020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: hgsc-help@bcm.tmc.edu
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----- Summary Statistics
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Unpublished
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Daly, M.J., Devon, K., Dewar, K., Forrest, C., Gage, D., Geraigery, K., Hagos, B., Harris, K., Huang, J., Hui, L., Jacotot, L., Kirby, A., Lane, M., MacKenzie, J., Marquis, N., McDermott, J., Molla, M., Morrow, J., Nachman, A., Naybor, J., Nubbaum, C., O'Connor, T., Morrow, J., Nachman, A., Naybor, J., Nubbaum, C., O'Connor, T., Stilwell, J., Stone, C., Strickland, C., Sydney, K., Tang, L., Wilmer, F., Zemtseva, I. and Zody, M.

Direct Submission

L. Submitted (06-JUN-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 4, 1997 this sequence version replaced gi:2085774.

The Staden databases, finishing information, and all chromatographic files used in the assembly of this clone are available from our anonymous ftp site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="4314"
/clone_lib="Research Genetics/Cal Tech CITB9785K-B (plates
1-194)"
                                                                                                                                                                                                                                                                                                                                                                                                                  All repeats were identified using RepeatMasker: Smit, A.F.A. Green, P. (1996-1997) this://ftp.genome.washington.edu/RM/RepeatMasker.html. LocationGoualIfiers
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/rpt_family"LINE2"
14837. .14904
/rpt_family"(CAGC)n"
complement(14906. .14963)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="(GA)n"
complement(7528. 7829)
/rpt_family="AAusx"
complement(A60)
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complement(1659. .1701)
/rpt_family="(CA)n"
2009. .2282
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9321. 9467
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985. .10210
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/rpt_family="MIR"
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/rpt_family="LINE2"
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2572. .12644
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/rpt_family="Alusx"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118. .660
rpt_family="MLT1C"
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1052, 11216
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Lutect Submisted (199-MAY-1997) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Hawkins,T.L., Birren,B.W., Fasman,K.H., Nussbaum,C., Lander,E.S., McKernan,K., Munro,C., Richardson,P., Barna,N., Charg,A., Cooke,P., Hagos,B., Harris,K., Huang,J., Hui,L., Jacotot,L., Kirby,A., Lane,M., MacKenzie,J., Marquis,N., Hui,L., Jacotot,L., Kirby,A., Cooke,P., Morrow,J., Nachman,A., Naylor,J., Nusbaum,C., O'Connor,T., Olotu,A., Peterson,K., Reeve,M.P., Roberts,D., Rollins,G., Stilwell,J., Stone,C., Strickland,C., Sydney,K., Tang,L., Nilmer,F., Zemtseva,I. and Zody,M.

Lumanited (02-SEP-1997) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

S (bases I to 13776)

MCKernan,K., Munro,C., Richardson,P., Barna,N., Chang,A., Cooke,P., Hagos,B., Harris,K., Huang,J., Hui,L., Jacotot,L., Kirby,A., Lane,M., MacKenzie,J., Marquis,N., Robermott,J., Molla,M., Morrow,J., Nachman,A., Naylor,J., Nusbaum,C., O'Connor,T., Olotu,A., Peterson,K., Reeve,M.P., Roberts,D., Rollins,G., Stilwell,J., Stone,C., Strakland,C., Sydney,K., Tang,L.,

Stilwell,J., Stone,C., Strakland,C., Sydney,K., Tang,L.,

Nilmer,F., Zemtseva,I. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chases 1 to 137769)
Hawkins, T.L., Reeve, M.P., Christoffersen, A., Birren, B.W.,
Hawkins, T.L., Reeve, M.P., Christoffersen, A., Marchand, R.,
Basman, K.H., Lander, E.S., McKernan, K., Munro, C., Richardson, P.,
Gage, D., Geraigery, K., Hagos, B., Jacotot, L., Lane, M., MacKenzie, J.,
Marquis, N., McDermott, J., Molloney, N., Morrow, J., Nachman, A.,
Naylor, J., O'Connor, T., Peterson, K., Rollins, G., Spencer, J.,
Stilwell, J., Stone, C., Strickland, C., Sydney, K., Wilmer, F. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (13-MAY-1997) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases I to 137769)
Hawkins.T.L., Reeve,M.P., Christoffersen,A., Birren,B.W., Fasman,K.H., Lander,E.S., McKernan,K., Munro,C., Richardson,P., Barna,N., Chang,A., Cooke,P., Daly,M.J., Forrest,C., Fripp,W.J., Gage,D., Geralgery,K., Hagos,B., Jacotof.L., Lane,M., MacKenzie,J., Marquis,N., McDermott,J., Moloney,N., Morrow,J., Nachman,A., Naylor,J., O'Connor,T., Peterson,K., Rollins,G., Spencer,J., Stilwell,J., Stone,C., Strickland,C., Sydney,K., Wilmer,F. and
                                                                                                                                                                                               PRI 06-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 137769)
Hawkins, L., Birren, B.W., Fasman, K.H., Nussbaum, C. and Lander, E.S. Genomic sequence from Human 17
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                                                                                                                                                                                                                     sequence from Human 17, complete sequence
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1011 tagcaacaatatgtcaacaaacatatgtgac 1041
                                                                                                                                                                                            137769 bp
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AC002090.1 GI:2160130
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                                                                                                                                                                                                                                                                                                                               SOURCE
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Submitted (04-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquifies: humquery@sanger.ac.uk Clone requests: clonerquest@sanger.ac.uk
on Sep 6, 2001 this sequence version replaced gi:14800199.
During sequence assembly data is compared from overlapping clones, where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chamistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; SW.; SWISSPROT: TT:, TREMBL; Wp:, WORNDEPP; Information on the WORNDEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group.
                                                                                                                                                                                                                                        AL139275 193126 bp DNA linear PRI 04-SEP-2001
Human DNA sequence from clone RPI1-552E20 on chromosome
6p12.3-21.2, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6 RP11-552E20 is from the library RPCI-11.2 constructed by the group Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                               1032 catatgigaccccaigaaaaciitaittaigaaacgaaaaccigaaaataagga
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/note="match: GSS: Em:AQ437688"
complement(8999. .9566)
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/note="match: GSS: Em:B71338"
4256. 4678
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/clone="RP11-552E20"
/clone_lib="RPC1-11.2"
12. .455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                 GI:15485119
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Direct Submission
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AL139275.30
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/note="Sequence in this region could not be obtained from
the other strand or with an alternative sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    972 cacaactactcatctctgcctctgtagcacgaaagcaattagcaacaatatgtcaacaaa 1031
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complement(35105..35297)
/rpt_family="MIR"
complement(35585..35766)
/rpt_family="MIR"
complement(36289..36589)
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complement(310998. .31061)
/rpt_family="LINE2"
complement(31629. .31659)
/rpt_family="AT_rich"
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26342 . 2647
/rpt_family"MRR"
26712 . 26929
/rpt_family"MRRSBA"
complement(7253 . 27327)
/rpt_family"MRR"
complement(28097 . 28886)
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23894. .24398
                                                                                                                                                                                                                                                                                                                 complement (22871. .22908)
/rpt_family-"AT_rich"
complement (23129. .23168)
/rpt_family-"LINE2"
                                   /rpt_family="AT_rich"
complement(19230, 19258)
/rpt_family="AT_rich"
complement(19446, 19742)
                                                                                             /rpt_family="Alur"
19749. 19785
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21555. .21640
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complement/?????
/rpt_family="LINE2"
complement(17782. .17841)
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34740. .35075
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29156. .29359
/rpt_family="L1"
30191. .30324
/rpt_family="MIR"
30411. .30728
                                                                                                                                                                                                                                                                         complement(21855
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26012. .26140
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33484. .347
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Complement(64900, .64983)

/note="match: GSS: Em:AZ237938"

/note="match: GSS: Em:AL191898"

64903, .64991

/note="match: GSS: Em:AL309316 Em:AL316981 Em:AL346021"

64903, .64991

/note="match: GSS: Em:AL309316 Em:AL316981 Em:AL346021"

/note="match: GSS: Em:AL224697"
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/hote="match: GSS: Em:AQ181384"
complement(77154, 77547)
/hote="match: GSS: Em:AQ192713"
80797, 81303
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64898. .65015. Em:A0932064"
/note="match: STS: Em:G09742"
/note="match: GSS: Em:A257084"
/complement(64898. .64989)
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(-64975)
(S: Em:AL324222"
(-64983)
                                                                                                                             complement(10116. .10617)
/note="match: STS: Em:G56076
match: GSS: Em:AQ318725"
13203. .13321
/note="match: GSS: Em:AQ792274"
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15417, .15794
/note="match: GSS: Em:AQ138303"
/note="match: STS: Em:G63453"
9829. 110237
/note="match: GSS: Em:AQ030932'
complement(10116. 10617)
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/note="match: GSS: Em:AL284370"
complement(64903. .64983)
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Em:G08189"
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4905. .65002
note="match: GSS: Em:AQ284087
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//octe-match: STS: Em:G0818
complement(64864. 64983)
//note-match: GSS: Em:AL328
complement(64864. 64975)
//note-match: GSS: Em:AL328
complement(64888. 64983)
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                                         misc_feature
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ORIGIN
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Query Match 3.9%; Score 90; DB 2; Length 177957; Best Local Similarity 57.1%; Pred. No. 5.9e-14; Matches 186; Conservative 0; Mismatches 135; Indels 5.
1829 1928: gap of 100 bp 1929 26477: contig of 24489 bp in length 26418 26517: gap of 100 bp 26518 54437: contig of 27920 bp in length 5438 54537: gap of 100 bp 5438 101424: contig of 46887 bp in length 101425 101524: gap of 100 bp 101525 177957: contig of 76433 bp in length.
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54538 .101424
/note="assembly_fragment"
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                                                                                                                                                                                                                                                            AC025298 177957 bp DNA linear HTG 03-JUN-2000
Homo sapiens clone RP11-2N21, WORKING DRAFT SEQUENCE, 5 unordered
                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 177957)
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: L2880
Center clone name: L2880
Center clone name: L2880
Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator But gpye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 174723 bases at least 040
Consensus quality: 177197 bases at least 030
Consensus quality: 177197 bases at least 020
Insert size: 182000; agarose-fp
Insert size: 0200
Unality coverage: 6.7 in 020 bases; sum-of-contigs
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Web site: http://www.seq.wi.mit.edu
Ontact: sequence_submissions@genome.wi.mit.edu
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                                                                                                                                                                                                              Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-2N21
Unpublished
                                                                                      AC025298.3 GI:8225254
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                               Homo sapiens
                                                         pieces
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     AC025298
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AC022801 178477 bp DNA linear HTG 17-MAR-2000 Homo sapiens chromosome 14 clone RPl1-354A24 map 14, WORKING DRAFT SEQUENCE, 13 unordered pieces.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                           829 ccactgagctggaggcagttatcctgtccccacgtcacattcctactcccgtttcccat 888
   Gaps
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10108 AGGTTCTATTGCTAGCTTTGCTACAAATGACCAAGACAAAGGTCAGTAAACTTTTTCTGT 100049
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                                                             96636 96735: gap of 100 bp 96736 120473: contig of 23682 bp in length 120418 120517; contig of 23682 bp in length 120518 149372: contig of 28855 bp in length 149373 149472: gap of 100 bp 149473 app of 100 bp 15085 bp in length 150873 178477: contig of 29005 bp in length 1.178477: contig of 29005 bp in length 1.178477
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21888. 31116
31217 ...39038
71017 ...39038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16910.
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Best Local Similarity
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                                                                                                                                                  Sirren, B. Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Colangalavkiy, L., Bouwhalter, B., Brown, A., Burket, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferrest, C., Gage, D., Galagan, J., Rerfara, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Karatas, A., Klein, J., Landcars, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, E., Morrow, J., Naylor, J., Norhman, C. H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassillev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Littel, S., Mand, C., Myman, D., Ye, W. J., Littel, A., Mand, L., Myman, D., Ye, W. J., Littel, A., Mand, L., Myman, D., Ye, W. J., Littel, A., Mand, L., Myman, D., Ye, W. J., Myman, D., Ye, W. J., Littel, Submission, M., Shands, M., Sandos, R., Walley, R., Vo, R., Wu, X., Wyman, D., Ye, W. J., Myman, D., Ye, W. J., W. J., Myman, D., Ye, W. J., W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 17, 2000 this sequence version replaced gi:6980319.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality coverage: 5.4 in Q20 bases; agarose-fp
Quality coverage: 5.5 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.seq.wl.mit.edu
Contact: sequence_submissions@genome.wl.mit.edu
Contact: sequence_submissions@genome.wl.mit.edu
Center project name: L6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 1693; contig of 1693 bp in length
1694 1793; gap of 100 bp
1794 4778; contig of 2285 bp in length
4079 4178; gap of 100 bp
11243; contig of 10065 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             p of 100 bp contig of 10649 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16: gap of 100 bp
39038: contig of 7822 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14244 14343: gap of 100 bp
14344 21787: contig of 7444 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              p of 100 bp
contig of 9229 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  p of 100 bp contig of 7671 bp in length
1 (bases 1 to 178477)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 14, clone RP11-354A24
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 bp
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21888 31116: cont
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46910 57558; con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57658: gap of
                                                                                                                           (bases 1 to 178477)
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      REFERENCE
AUTHORS
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                                                                                                                                                           AUTHORS
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TITLE

COMMENT

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us-09-515-369b-1.rge

DEFINITION RESULT 13 AC098645

ACCESSION

VERSION

ORGANISM

KEYWORDS SOURCE

REFERENCE

AUTHORS

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181009 bp DNA linear HTG 12-MAR-2000 Homo sapiens clone RP11-11G16, WORKING DRAFT SEQUENCE, 25 unordered AC011060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db.138355 CCCCAGCCTAGAGTAGAAGTGCCAAAGTTCTCTTGTAAAGAGCCAGACAGTGAATATT 138414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DD 138535 ATGGACGTGAAATTCTGGAGTTGCAAATAATTC---TCACATTTTTTCCAACCATTAAAAA 138591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 138415 TTGGCTTCGTGGGCCCGATCAGCTCTATCACAACTACTCAACTCGCCATTGTAGCACAA 138474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1004 aagcaattagcaacaatatgtcaacaaacatatgtgaccccatgaaaactttattatta 1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1064 tggatacggaaacctgaaaataatgtctttcttttgatttttccccaatcattaaaaaa 1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.28.29. .100592
/note="assembly_fragment"
100693. .159516
/note="assembly_fragment"
147682. .192695
/note="clone overlaps with GenBank Accession Number
AC096698 clone RP41-177A23 (center project name csc)"
159617. .192695
/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  884 cccatgcctggacccaggttgggcaaactcttcctgtaaagaaccagacaggaactattt 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vector_side:left"
1. .65403
Anotes clone overlaps with GenBank Accession Number Accession Tolone RP41-327F23 (center project name csa)" 31268. .72728
Query Match 3.9%; Score 90; DB 2; Length 192695; Best Local Similarity 62.0%; Pred. No. 5.9e-14; Matches 160; Conservative 0; Mismatches 95; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    411 others

    192695
/organism="Papio cynocephalus anubis"
//db_xref="taxon:9555"
/clone="RP41-470J23"

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| 40608 c 37486 g 55595 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RP41"
1. 31167
/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone_end:SP6
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                  SM Papio cynocephalus anubis
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota: Metazoa; Chordata; Catarrhini; Cercopithecidae;
Cercopithecinae; Papio.

I (bases 1 to 192695)
S Akhter, N., Agels, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighl, P.,
Ho, S.-L., Idol, J.N., Karling, E., Lartc, P., Lee-Lin, S.-Q.,
Legaspi, R., Maduro, Q.L., Maduro, V.B., Masiello, C., Maskeri, B.,
Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A.,
Stantipop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W.,
Young, A., Zhang, L.H., and Green, B.D., Waigins, L.,
Young, A., Zhang, L.H., and Green, B.D., Waigins, L.,
                                                                                                                                              HTG 01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence data in units record represents an enhanced version of a phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assemblist based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblist, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

Sequencing vector: plasmid; n/s, 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 191690 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submission
Submission
Submitted (27-OCT-2001) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
On Feb 1, 2002 this sequence version replaced gi:16506407.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
      9868 AATATTATTCGTTTTTCCCAATCATTAAAACATATAAAAACCACTCTTAAGTCACA 9813
                                                                                                                      ACU98645 192695 bp DNA linear HTG Ol-
Papio cynocephalus anubis clone RP41-470J23, WORKING DRAFT
SPOUENCE, 5 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert size: 182000; agarose-fp
Insert size: 192295; sum-of-contigs
Quality coverage: 10.92x in Q20 bases; agarose-fp
Quality coverage: 10.33x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence data in this record represents an 'enhanced'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. Gaps between the contigs. * are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: NIH Intramural Sequencing Center
Center code: NISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: csb
Center clone name: 470J23
                                                                                                                                                                                                                                                            AC098645.2 GI:18464060
HTG; HTGS_PHASE2; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 192695)
                                                                                                                                                                                                                                                                                                                        olive baboon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Green, E.D.
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TITLE JOURNAL

COMMENT

AUTHORS

TITLE JOURNAL REFERENCE

3;

ORGANISM

VERSION KEYWORDS SOURCE REFERENCE AUTHORS TITLE JOURNAL REFERENCE

AUTHORS

TITLE JOURNAL

COMMENT

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118 2017; gap of 110 by 110 by 12215; gap of 1100 by 1116 22215; contig of 1998 by in length 116 22215; gap of 100 by 100 by 12215; gap of 100 by 100 by 12556; contig of 2212 by in length 157 24556; gap of 100 by 12527; gap of 100 by 13252; contig of 5265 by in length 138 37892; contig of 5265 by in length 138 37892; contig of 5265 by in length 138 37892; gap of 100 by 100 by 11055; gap of 100 by 11035 by in length 166 41365; gap of 100 by 11035 by in length 16500; gap of 100 by 11035 by in length 16500; gap of 100 by 11006 by 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149438 149437: gap of 100 bp
149438 181009: contig of 31572 bp in length.
Location/Qualifiers
1. 181009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              up of 100 bp contig of 15756 bp in length
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97023: contig of 17561 bp in length
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                                                                                                                                                                                87: gap of 100 bp
15707: contig of 1520 bp in length
                                                                                                                                                                                                                                                          contig of 2138 bp in length
                                                                                                                                                                                                                                                                                                                                    oof 100 bp
contig of 1972 bp in length
                                                                     bp in length
                                                                                                                                               1788 bp in length
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1. .1504
                                                                                                      100 bp
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4010, 5556
/note="assembly_fragment"
5657, 7482
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/note="assembly_fragment"
9027, .10470
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/note="assembly_fragment"
2892, .3909
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/note="assembly_fragment"
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/db_xref="taxon:9606"
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v: gap of
12199:
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20017: cont
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Direct Submission

Submitted (30-SEP-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 12, 2000 this sequence version replaced gi:6984405.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatWasker:
                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 181009) Briren, E., Linton, E., Nusbaum, C., and Lander, E. Homo saplens, clone RP11-11616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Whitehead Institute/ MIT Center for Genome Research
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Sequencing vector: N13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 175981 bases at least Q40
Consensus quality: 175073 bases at least Q30
Consensus quality: 175479 bases at least Q20
Insert size: 155000; agarose-fp
Insert size: 155000; agarose-fp
Quality coverage: 5.1 in Q20 bases; agarose-fp
Quality coverage: 5.1 in Q20 bases; sum-of-contigs
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contig of 1547 bp in length
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Center clone name: 11_G_16
                    AC011060.5 GI:7229784
HTG; HTGS_PHASE1; HTGS_DRAFT
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4010 5556; conf
5657 656; gap of
7482; conf
7483 7582; gap of
7583 8926; conf
9027 10470; conf
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Location/Qualifiers
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/note="match: GSS:
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ALIG1628 GI:10129841
HTG; CpG island; ELAVL2; snoRNA binding domain.
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Direct Submission

Submitted (20-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk

On Sep 14, 2000 this sequence version replaced gi:10039694.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 183483)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 151319 CTAGCACACACGACGTCAGCAAACTTTCTCTGTAAAGGACCAGATGATAAAATATTTTAGGTTT 151378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 89.2; DB 2;
Pred. No. 9.9e-14;
0; Mismatches 73;
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                                                                                                                       41366. 52400
/note-"assembly_fragment"
52501. 63506
/note-"assembly_fragment"
63607. 79362
/note-"assembly_fragment"
                                                                                                                                                                                                                                                                79463 97023
/note="assembly_fragment"
97124. 124426
/note="assembly_fragment"
124527. 149337
/note="assembly_fragment"
149438. 181009
/note-"assembly_fragment" 3268. 31892 /note-"assembly_fragment" 37993. 41265 /note-"assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                         /note="assembly_fragment"
a 36532 c 33173 g 51292
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                                                                                                    vector_side:right"
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                                                                                       clone_end:SP6
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Group. Purther information can be found at http://www.sanger.ac.uk/HGP/Chr9
This sequence is the entire insert of clone RP11-31K16 The true left end of clone RP11-31L2 is at 139671 in this sequence. The left end of clone RP11-31L3 is at 13045 in this sequence. The true right end of clone RP11-31S114 is at 73045 in this sequence. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence feature key. RP11-31K16 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Emm., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at
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//note="MLTI repeat: matches 343, .398 of consensus" 5387. .5466
//note="MEMS repeat: matches 2214. .2294 of consensus" 5639. .5786
//note="LIME3A repeat: matches 6017. .6156 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="L1MC2 repeat: matches 4721. .6314 of consensus"
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764. .954
760-**AluJo repeat: matches 118. .297 of consensus"
1096. .1173
7note="MLTIJ repeat: matches 103. .187 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note. MER58B repeat: matches 46. .341 of consensus. 11076. .11221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .2412 of consensus"
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/note="MEREA repeat: matches 2. .120 of consensus"
/note="L2 repeat: matches 2252. .2736 of consensus"
7345. 7344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MLT2CB repeat: matches 1. .504 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              415. .471
/note="AluJo repeat: matches 60. .118 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7437. 7741
/note="AluSx repeat: matches 1. .299 of consensus"
7808. .7989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="AluY repeat: matches 10, ,288 of consensus"
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/note="MER20 repeat: matches 1, .218 of consensus"
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11222. .11661
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10366, .10649
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/note="match: GSS: Em:AQ040596"
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/db_xref*"taxon:9606"
/chromosome="9"
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/clone_lib="RPCI-11.1"
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.6165 of consensus"
.510 of consensus"
                                            consensus
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30582. .30732
Anote-"MER5A repeat: matches 8. .187 of consensus"
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/ note="MER30 repeat: matches 1. .230 of cot complement(23139..2350)
/ note="MIR repeat: matches 119..246 of cot complement(23139..2350)
/ note="match: GSS: Em:AQ210496"
/ note="match: GSS: Em:AQ210496"
/ note="match: GSS: Em:AQ10496"
/ note="MSTD repeat: matches 1. .341 of cons 27203..2769
/ note="MSTD repeat: matches 1. .341 of cons 27203..27760
/ note="MSTD repeat: matches 341..394 of cc 27696..27750
/ note="MSR5A repeat: matches 34..189 of co 2786..27750
/ note="MSR5A repeat: matches 3..183 of con 28766..29329
/ note="match: GSS: Em:B93338"
/ note="match: GSS: Em:AQ125799"
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/note="33 copies 2 mer aa 71% conserved"
29763. .29807
/note="9 copies 5 mer aaaac 82% conserved"
30205. .30412
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                                                                                                                                                                                                                                                                                                                                       complement(17116. .1755)
/note="match: GSS: Em:AQ133240"
/17546. .18050
/note="match: GSS: Em:AQ777145"
/1760. .17960
/note="match: GSS: Em:AQ094704"
/19777. .19993
/note="match: GSS: Em:AQ376698"
/note="match: GSS: Em:AQ376698"
/note="match: GSS: Em:AQ376698"
/note="match: GSS: Em:AQ376698"
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/note="match: GSS: Em:AQ235822"
complement(20830. 21137)
/note="match: GSS: Em:B65379"
21100. 21154
/note="11 copies 5 mer aaaac 78%
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/note="match: GSS: Em:AQ546895"
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6, 2002, 12:16:57

Search completed: June Job time: 14004 sec

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.171992))
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//Octe="match: CDNAs: Em:U29088 Em:X85111 Em:M62843

Em:U17602 Em:U12431 Em:L26405 Em:U17599 Em:U29148

Em:U17597 Em:D26158 Em:S83320 Em:D31953 Em:AF176675

Em:AA545382 Em:AA081894 Em:AR41112

Em:AA656788 Em:AA692890 Em:A1143457 Em:AN411363

Em:AA656788 Em:AA61369 Em:A1144457 Em:AN411363

Em:AA56778 Em:AA416369 Em:A1144457 Em:AN491188
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                                                                                                                                                                                                                                                                                                       /note="ballki6.1 (snoRNA binding domain pseudogene)
match: proteins: Sw:000567 Tr:099M69 Tr:092RW0 Tr:099D11
Tr:094514 Sw:021276 Tr:095GT7 Tr:029158 Sw:012460
Tr:080401 Tr:065334 Tr:065335 Tr:09U5W4"
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/evidence=not_experimental
34066...34977
/note="AluSg repeat: matches 11. .297 of consensus"
36947...36978
/note="16 copies 2 mer aa 87% conserved"
38608...39160
/note="match: GSS: Em:AQ353745"
                                                                        consensus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.9%; Score 89.2; DB 9; Length 183483; Best Local SImilarity 64.6%; Pred. No. 9.9e-14; Matches 133; Conservative 0; Mismatches 73; Indels 0;
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                                                                        . 206
32009. .32080
/note="MIR repeat: matches 132,
32125. .32784
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                                                                                                                       /gene="bA31K16.1"
32125. .32704
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Human melanoma dif	Human immune/haema	Human immune/haema	Human cDNA sequenc	Human musculoskele	Human immune/haema	Human PP1345 prote	Human EST-derived	Human secreted exp
SUMMARIES	ai	AAH26595	AAK84165	AAK84166	AAH14600	AAL36313	AAK74761	ABA04430	AAH98619	AAA41353
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Melanoma differentiation associated gene-7 promoter capable of treating cancer comprises directing transcription of heterologous coding sequence encoding tumour suppressor polypeptide positioned
                                                                                                                                                                                                                                                                 downstream, useful for treating cancer
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                                                        "C/EBP
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The present sequence is that of the promoter region of the human melanoma differentiation associated gene-7 (Mda-7). It includes 2240 bp from the 5' flanking region of the Mda-7 gene. The promoter was isolated from a human placental genomic library using a PCR-based method. The Mda-7 promoter exhibits melanocyte tissue, i.e. the skin. Therefore, a gene of increst driven by the Mda-7 promoter will be differentially expressed in these cells, animalising systemic toxicity. A recombinant expression construct in which the human Mda-7 promoter is operably linked to a coding sequence encoding a tumour suppressor protein is claimed. The tumour suppressor is preferably p21, retinoblastoma protein or p53. A host cell comprising the expression construct is also claimed, and is preferably a tumour cell selected from a melanoma, neuroblastoma, astrocytoma, glioblastoma multiforme, cervical cancer, breast cancer, lung cancer or prostate cancer cell. The promoter preferably comprises nucleotides 1-2240 of the present expression including the recombinant expression construct is also claimed. Sequence or profession including the recombinant ', prostate cancer, the central nervous sequence. A pharmaceutical composition including with sequence. A pharmaceutical composition including method of treating melanoma, neuroblastoma, astrocytoma, glioblastoma multiforme, cervical cancer, breast cancer, colon cancer, prostate cancer, osteosarcoma, chondrosarcoma or a cancer of the central nervou

Gaps Length 2286; ö Indels Sequence 2286 BP; 547 A; 592 C; 510 G; 637 T; 0 other; 22; DB Mismatches 100.0%; Score 2286; 100.0%; Pred. No. 0; ö Query Match 100. Best Local Similarity 100. Matches 2286; Conservative

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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to provent, diagnose and treat immune/haematopoletic-related diseases, especially cancers and cancer metastases of haematopoletic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoletic antigen genomic sequences from the present invention. AAK84942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32270 AAATTGTCCTTTGCAATGGTCAGATATCTAACACAGGGGTCAGCAAACTTTTTCTGAAAA 32211
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                                                                              2000US-0249264.
2000US-0249265.
2000US-0249297.
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2000US-0249300.
2000US-0250160.
2000US-0250391.
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                                                          2000US-0249245
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Best Local Similarity
Matches 144; Conserv
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-NOV-2000;
   Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                     Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38978
 ВР
                                                                                  AAK84166/c
ID AAK84166 standard; DNA; 37442
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20000S-0190076
20000S-0190123
20000S-0209467
20000S-021886
20000S-0215135
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20000S-021647
20000S-0216880
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AAK54951 to AAK64702 encode the human immune/haematopoletic antigen (1) amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) to polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to provent, diagnose and treat immune/haematopoletic-related diseases, especially cancers and cancer metastases of haematopoletic darigen genomic sequences from the present invention. AAK59401 to AAK87691 metastases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           represent sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 38978; 3071pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                           Ruben SM;
                                                                 20000S-0251030.
20000S-0251988.
20000S-025198.
20000S-0251479.
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20000S-0251868.
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                            01-DEC-2000;
01-DEC-2000;
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32329 TCCACTTCATTCTTTCATGTCTACTTTCCAGTATATTTCCTAAAAACAACATAAAA 32270
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3.6%; Score 81.4; DB 22; Length 37442; 53.0%; Pred. No. 2.2e-12;
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                                              81; Indels
                                              0; Mismatches
                        Best Local Similarity 63.0%;
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AAH14600 standard; cDNA; 5294 BP

RESULT 4
AAH14600/c
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The present invention describes primer sets for synthesising 5602 (ull-length cDNAs defined in the specification. Where a primer set comptries: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 3'-end sequence complementary to the complementary strand of a polynucleotide which comprises a 1'-end sequence. Onlynucleotide which comprises a 3'-end sequence of sequence of the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs assily without any specialised methods. AMR03166 to AMH18628 and AMH18633 to AMH1872 represent human cDNA sequences.
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                                                                                                                                    Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss
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Otsuki
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llarity 74.5%; Pred. No. 9.5e-13;
Conservative 0; Mismatches 35;
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Ishii S, Sugiyama T, Wakamatsu A, Nagal K,
                                                                                             Human cDNA sequence SEQ ID NO:12215.
                                                                                                                                                                                                                                                                                                                                                   27-Aug-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
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                  AAH14600;
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21-SEP-2000;
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29-SEP-2000;
   antial....., immunosuppressive; nootropic; neuroprotective; antiviral; antializantialic antializabetic; antifilammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein;
  1855 GGGCCATATGGTCTCTGTGGCAATTACTTAACTCTGCCATCATAGCACGAAAGCAGCTAC 1796
                                                                                                                                              Human musculoskeletal system related polynucleotide SEQ ID NO 2678
                                                                            AAL36313/c
ID AAL36313 standard; DNA; 26591 BP
                                                                                                                                                                                                                                                                                                            2000US-0179065.
2000US-0180628.
2000US-018664.
2000US-0186350.
2000US-019076.
2000US-0190176.
2000US-0190123.
2000US-0205515.
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2000US-0215135.
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2000US-0225266
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2000US-0228924
                     1014 caacaatatgtcaacaa 1030
                                      1795 AGACAATATGTAGGGAA 1779
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                                                                                                                            (first entry)
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16-MAR-2000;
17-MAR-2000;
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14-JUL-2000;
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26-JUL-2000;
14-AUG-2000;
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19-MAY-2000;
07-JUN-2000;
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22-AUG-2000;
22-AUG-2000;
22-AUG-2000;
33-AUG-2000;
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01-SEP-2000;
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05-SEP-2000;
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24-FEB-2000;
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23816 AGAAAATATGAAAACAAATGGACGTGAC 23789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23936 GAGCAGGGGTTAGCAAAATTTTCTGTCTAGAGTCATATAGTAAATTTTTAAACTCTGC 23877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wlpo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                          Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.
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Pred. No. 2.4e-11;
0; Mismatches 44; Indels 0;
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                      2000US-0249244.
2000US-0249245.
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2000US-0249265.
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Best Local Similarity 70.3
Matches 104; Conservative
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Human; immune; haematopoletic; immune/haematopoletic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                          Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29573.
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AAK74761 standard; DNA; 481
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16-MAR-2000;
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                              AAK74761;
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08-SEP-2000; 2000US-0232080.
08-SEP-2000; 2000US-0232081.
14-SEP-2000; 2000US-023299.
14-SEP-2000; 2000US-023399.
14-SEP-2000; 2000US-023399.
14-SEP-2000; 2000US-023399.
14-SEP-2000; 2000US-023399.
14-SEP-2000; 2000US-0233063.
14-SEP-2000; 2000US-0233063.
14-SEP-2000; 2000US-0233063.
14-SEP-2000; 2000US-0233063.
15-SEP-2000; 2000US-0234091.
25-SEP-2000; 2000US-0234997.
25-SEP-2000; 2000US-0234997.
25-SEP-2000; 2000US-0234991.
26-SEP-2000; 2000US-0234991.
26-SEP-2000; 2000US-0234991.
26-SEP-2000; 2000US-0234991.
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I)

proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased cypression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I)

cuplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inscrting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic may be used to prevent, diagnose and treat immune/haematopoietic actived cells. AAK64703

connects and cancer metastases of haematopoietic antigen genomic to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK84950 and AAM82169

crepresent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis
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                                                                        2000US-0251988.
2000US-0256719.
2000US-0251479.
2000US-0251856.
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2000US-0251869.
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05-JAN-2001; 2001US-0259678.
2000US-0249300
                                    2000US-0250391.
2000US-0251030.
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Best Local Similarity 68.99
Matches 104; Conservative
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01-08C-2000;
05-08C-2000;
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06-08C-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                     suppressing activity. The present invention also describes a method for the preparation of the protein by recombination, and the application of the protein in treating diseases such as cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                      1699 tattcagototgotattgtaatacaaaagcagotgtggacagtatgtaaatgaatgaatg 1758
                                                                                                                                                                                                                                                                                                                                                                                                            tgtaaagaaccagacaggaactattttaggctctgtgtgccatatggtctcagtcacaac 977
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                              The present sequence encodes human PP1345 protein, which has cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition; ss.
                                                                                                                                                                                                                                               New \mbox{\sc human} protein able to suppress growth of cancer cells and its encoding polynucleotide sequence -
                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                      Length 1837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1038 tgaccccatgaaaactttattattatggatacggaaacctgaaaataa 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60; Indels
                                                                                                                                                                                                                                                                                                                                            Sequence 1837 BP; 478 A; 471 C; 407 G; 481 T; 0 other;
Human PP1345 protein encoding cDNA SEQ ID NO:19/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human EST-derived coding sequence SEQ ID NO: 476.
                                                                                                                                                                                                                                                                                                                                                                       Score 73; DB 24;
Pred. No. 1.2e-10;
                                                                                                                                                                                                                                                                            Claim 5; Page 33 (Disclosure); 42pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                    33
                                                       Location/Qualifiers
174..566
/*tag= a
                  Human; PP1345; cancer suppression;
                                                                                    /product- "PP1345"
                                                                                                                                                                                 (SHAN-) SHANGHAI INST ONCOLOGY
                                                                                                                                                                                                                                                                                                                                                                       3.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH98619 standard; cDNA; 628
                                                                                                                                                              13-MAR-2000; 2000CN-0111989
                                                                                                                                           13-MAR-2000; 2000CN-0111989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.29
Best Local Similarity 64.59
Matches 109; Conservative
                                                                                                                                                                                                                     WPI; 2002-042193/06.
                                                                                                                                                                                                                               P-PSDB; ABB04713
                                                                                                                                                                                                   Gu J, Yang S;
                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-OCT-2001
                                                                                                       CN1313315-A
                                                                                                                         19-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH98619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
AAH98619/C
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The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1074 aacctgaaaataatgtctttttttttttttttcccaatcattaaaaaacgtaaaact 1133
275 TTCACATAAAATATTTTTTTTTTTTTTTCCCCAACAATTAAAAATTTTAAAGCC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                954 gigccataiggictcagicacaactactcaictcigccicigiagcacgaaagcaaitag 1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1014 caacaatatytcaacaaacatatytgaccccatgaaaactttatttattatggatacyga 1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGACCATATGGTCTC--TGCTAACTACTCAATTCTGCCATTGAAGTGCAAAAGCAACCAT 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     894 gacccaggttggggcaaactcttcctgtaaagaaccagacaggaactattttaggctctgt 953
                                                                                                                                                                                                                                                                                                                                                                                                              Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; mouse; xenopus; rat; secreted expressed sequence tag; sEST; expressed sequence tag; EST; probe; chemotactic; proliferative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334 GTA-AATGAATGTACGTGGCTGTGTTTATTTGTGGACACTGAAATTTAAATTTCATAATT
                                                                                                                                                                                                                                                    Asundi V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
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                                                                                                                                                                                                                                                    Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 628 BP; 190 A; 122 C; 131 G; 185 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted expressed sequence tag SEQ ID NO:93.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 71.6; DB 22;
Pred. No. 1.7e-10;
                                                                                                                                                                                                                                                    ou P, Qian XB, Wang Z,
Zhang J, Werhman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 514; 1275pp; English.
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                                                 2000US-0491404.
2000US-0617746.
2000US-0631451.
2000US-0663870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.1%;
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25-JAN-2001; 2001WO-US02687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                       Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 151; Conservative
                                                                                                                                                                                                                                                                                 Drmanac RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                  WPI; 2001-476164/51
P-PSDB; AAM23960.
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                                                                                                                                                                                               (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                       Liu C,
                                                                              17-JUL-2000; 2
03-AUG-2000; 2
15-SEP-2000; 2
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                                                    25-JAN-2000;
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us-09-515-369b-1.rng

89 ATATEGICICICICCCCAACIACACACICCICCTCTTGIGIAAAAGCAGCAATAGACA 30

AAA1261 to AAA43419 represent specifically claimed secreted expressed sequence tags (SESTs), isolated from human, mouse, xenopus and rat tissues sources. The SESTs can have a range of activities depending on the tissues they were isolated from. The activities depending on chemotactic; proliferative; immunomodulatory; haematopoletic; chemokinetic; analgesic; haemastatic; thrombolytic; antilnflammatory; chemokinetic; antibacteria; antilufungal; antilufungal; antiluflammatory; antiacthmatic; vulnerary; antillcer; osteopathic; neuroprotective; nootropic; antiparkinsonian; antilorer; osteopathic; neuroprotective; anticonvulsant; and antildepressnt. The SESTs can be used for gene therapy and in vaccines. The SESTs are useful as probes for the molecules which correspond to the sESTs. Proteins encoded by the SESTs are useful in assays for determining biological activity and raising antibodies. They may be useful for treatment of autoimmune disorders (multiple sclerosis, insulin dependent diabetes), allergic conditions (atthma), myelodd or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation disorders (haemophilia, thrombosis), inflammatorry disorders (Crohn's disease), tumours, bacterial, fungal or viral infections, depression and psoriasis. AAA43420 to AAA43425 represent linker variants which are given immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal; antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian; Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (SESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders antiulcer; osteopathic; neuroprotective; noctropic; antipsoriatic; cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine; autoimmune disorder; multiple sclerosis; allergic condition; insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer; lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke; parkinson's disease; Huntington's disease; coagulation disorder; haemophilia; thrombosis; inflammatory disorder; Crohn's disease; Evans C; Collins-Racie LA, in the exemplification of the present invention. tumour; infection; depression; psoriasis; ss. LaVallie ER, Claim 1; Page 198; 618pp; English. 99WO-US24205. 98US-0104435 (GEMY ) GENETICS INST INC. Treacy M; WPI; 2000-317937/27. WO200021990-A1. Homo sapiens 15-OCT-1999; 15-OCT-1998; 20-APR-2000. Merberg D, Jacobs K, 

Sequence 286 BP; 88 A; 63 C; 50 G; 85 T; 0 other;

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1007 caattagcaacaatatgtcaacaaacatatgtgaccccatgaaaactttattattatgg 1066

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ö atatggtctcagtcacaactactcatctctgcctctgtagcacgaaagcaattagcaaca 1018 899 aggitgggcaaactcitccigtaaagaaccagacaggaactaitttaggcicigigigcc 958 Gaps 149 AGGCCAGATAAACTTTTTCTGTAAAGAGTCAGACAGTAAATATTTTAGGCCTGGTGGTCC 90 ô 3.1%; Score 71.4; DB 21; Length 286; 72.1%; Pred. No. 1.2e-10; Live 0; Mismatches 36; Indels 0 93; Conservative Query Match Best Local Similarity Matches 93; Conserv 956 g ò

The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dr primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer bown sequences have been obtained, the full 5' URR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss. in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design getetgtgtgccatatggtctcagtcacaactactcatetctgcctctgtagcacgaaag 1006 887 atgcctggacccaggttgggcaaactcttcctgtaaagaaccagacaggaactatttag 946 Gaps diagnostic, forensic, gene therapy and chromosome mapping procedures New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for 2; Length 407; Indels Sequence 407 BP; 118 A; 72 C; 84 G; 127 T; 6 other; 3.1%; Score 71.2; DB 21; 63.6%; Pred. No. 1.7e-10; Live 0; Mismatches 69; Human secreted protein 5' EST, SEQ ID NO: 31863 Duclert A, Giordano J; Claim 1; SEQ ID 31863; 71pp + CD-ROM; English expression and secretion vectors. AAC27788 standard; cDNA; 407 BP 21-FEB-2000; 2000EP-0200610. 99US-0122487 (first entry) Matches 124; Conservative Dumas Milne Edwards J, Similarity WPI; 2000-500381/45. 1019 atatgtcaa 1027 29 ATATGTAAA (GEST ) GENSET 26-FEB-1999; Homo sapiens. EP1033401-A2. 06-OCT-2000 06-SEP-2000. AAC27788; Query Match Best Local RESULT 10 947 AAC27788/c ò d δ a ŏ qq NAMES OF STREET OF STREET

17555 ac 17556

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Aminopeptidase; human; AmP; gene therapy; treatment; AmP-deficiency; prenatal diagnosis; angloedema; antihypertensive agent; atherosclerosis; arterial stenosis; industrial protein feed; malabsorption syndrome; proteinaceous waste degradation; additive; immunohistochemistry; ss.

aminopeptidase P genomic DNA fragment 1.

Human kidney

Homo saptens W09911799-A2

(first entry)

BP.

AAX23517 standard; DNA; 50000

AAX23517

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Thu Jun

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genes involved in central nervous system (CNS) disorders (see AAH88161-AAH88702). The markers have a single nucleotide polymorphism (SNP) and are useful in determining the genetic predisposition of individuals to CNS disorders, by identifying the nucleotides at a set of genetic markers in a biological sample, where the markers comprise at least one CNS disorder related marker. The present sequence was used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acceaggitgggcaaactetteetgtaaagaaceagacaggaactatttaggetetgtg 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to biallelic markers derived from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated polynucleotides, useful for genotyping nucleic acids for biallelic markers for the diagnosis of depression, comprises central nervous system disorder related biallelic marker -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 123219 BP; 27921 A; 32327 C; 32369 G; 30437 T; 165 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23; Length 123219;
                                                                                                                                                                                                                                                          Single nucleotide polymorphism; SNP; biallelic marker; human; central nervous system disorder; CNS; ds.
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le-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 70;
Pred. No.
                                                                                                                                          AAH88703 standard; DNA; 123219 BP.
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                                                                                                                                                                                                                               Human DNA sequence SEQ ID 543.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cohen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                       11-JAN-2001; 2001WO-IB00116.
                                                                                                                                                                                                                                                                                                                                                                                                                    13-JAN-2000; 2000US-0175854.
                                                                                                                                                                                                  (first entry)
                                        1067 atacggaaacctgaa 1081
                                                                   224 ACATTGAAATTTGAA 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chu T, Blumenfeld M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-483085/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                               WO200151659-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                               (GEST ) GENSET
                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                  26-FEB-2002
                                                                                                                                                                                                                                                                                                                                                            19-JUL-2001,
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                                                                                                                                                                       AAH88703;
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Nucleic acid encoding human aminopeptidase P

(MEDI-) MEDICAL COLLEGE GEORGIA RES INST,

Sprinkle TJC,

Ryan JW,

WPI; 1999-205193/17.

98WO-US18426 97US-0057854

02-SEP-1998; 02-SEP-1997;

11-MAR-1999

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in cases of excessive Amp expression. The product of the invention is also used to identify Amp-expression. The product of the invention is generate transgenic animals, and comparisons of genomic sequences are used to detect mutations. Amp inhibitors are potentially useful as antihypertensive agents and to prevent or treat arterial (re)stenosis antihypertensis. The structure of Amp is used to design synthetic substrates, e.g. for use in Amp assays. Amp, which hydrolyzes N-terminal imido bonds, can be used to degrade industrial protein feeds to free formulations used to degrade proteinaceous wastes, as additives in enzyme formulations used to treat malabsorption syndrome and for studying its biological role. Antibodies against Amp are used in immunohistochemical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AmP). This protein is used to produce recombinant AmP and can be used for gene therapy for treating AmP-deficiency conditions. Its fragments are used as primers and probes to identify patients with homosygous and beterozygous AmP deficiency, including prenatal diagnosis (patients defective in AmP are at risk of developing angloedema if treated with anglotensin-converting enzyme inhibitors), also as antisense inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention describes the isolation of a novel human aminopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gcctggacccaggttgggcaaactcttcctgtaaagaaccagacaggaactattttaggc 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.1%; Score 69.8; DB 20; Length 50000; 72.7%; Pred. No. 7e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 13; Page 80-109; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to study AmP distribution.
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tgccatatggtctcagtcacaactactcatctgcctctgtagcacgaaagcaattagc 1014

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianemaic, antiaggregant; haemostatic; vulnerary; antidabetic; osteopathic; dermatological; antialergic; antiasthmatic; antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; and immunostimulant. The proteins and polymucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production, The proteins and polymucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, anaemia, platelet disorders, thrombotycopaenia, wounds, burns, ulcers, osteoporosis, severe combined immunodeficiency, eczema, allergic
                                                                                                                                                                                                                                             Human; cancer; ulcer; HIV infection; human immunodeficiency virus; antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anemaiagnegant; haemostatic; vulnerary; antiulcer; osteopathic; eccema; dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancrealtis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoietic disorder; platelet disorder; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM99166 to AAM99904 encode the human proteins given in AAM25225 to AAM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antlinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                   thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
                                                                                                                                                                                                                   Human protein encoding cDNA sequence SEQ ID NO:582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 622-624; 1217pp; English
1009 attagcaacaatatgtcaacaaa 1031
                   AAH99747 standard; cDNA; 8029
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2000US-0488725.
2000US-055317.
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                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neurological disorder; ss.
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21-JAN-2000;
25-APR-2000;
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                                                                                                                                                                                    Gaps
rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, Alzheimer's disease, Parkinson's disease, neurodegenerative and
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                                                                                                                                                                                                                                                                                                                                                                                                                           802 caataccataaatgaatgggtgtggctatgctctaataacattttgtttatggacactga
                                                                                                                                                                                                                                                                                                                          DNA encoding Aldehyde dehydrogenase 5 family, member Al (ALDH5Al).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aldehyde dehydrogenase 5 family member Al; ALDH5Al; succinate-semialdehyde dehydrogenase; gene therapy; probe; antisense technology; allele specific oligonucleotide; ASO; d-hydroxybutyric aciduria; metabolic disease; transgenic animal; chromosome 6p22; ds.
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                                                                                                                                          Length 8029;
                                                                               Sequence 8029 BP; 2064 A; 1942 C; 1905 G; 2118 T; 0 other;
                                                                                                                                                                                  Indels
                                                                                                                                        3.0%; Score 69.4; DB 22;
57.2%; Pred. No. 3.2e-09;
                                                                                                                                                                                  0; Mismatches 121;
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replace(3749,T)
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replace(3941,T)
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                                       neurological disorders.
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Matches 202;
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The invention describes an isolated polynucleotide comprising a nucleotide sequence which is a polymorphic variant of a reference sequence for the aldebyde dehydrogenase 5 family, member Al succinate-semialdehyde dehydrogenase) (ALDH5Al) gene or its fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New genetic variants of human aldehyde dehydrogenase 5 family, member Al, ALDH5Al gene for treating metabolic diseases and for expressing ALDH5Al protein useful in identifying drugs to treat 4-hydroxybutyric aciduria
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/standard_name= "Single nucleotide polymorphism"
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/*tag= as
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29454..29597
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31820..31978
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11231..42559
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replace(42380,T)
                                     replace(29397,T)
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41172..41230
/*tag=_ ar__/num
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37220..41171
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/number= 5
24598..31819
/*tag= ae
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37050..37219
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P-PSDB; AAU73594.
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 /note= "Aldehyde dehydrogenase 5 family member Al
Specifically claimed in claim 25"
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11876..11659
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/standard_name= "Single nucleotide polymorphism"
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13922..14038
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14039..24219
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replace(4179,G)
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replace(13855,G)
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replace(4155,C)
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                                            'product "ALDH5Al"
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                                                                          replace(4059,G)
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/*tag= q
/number= 3
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11660..12315
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                            4050..42765
/*tag= h
4050..4403
/*tag= 9
/number= 1
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The polypeptide is useful for screening for drugs targeting it by contacting the ALDHSAL polymorphic variant with a candidate agent and sassaying for binding activity. The polypeptide and haplotypes are useful for identifying an association between a trait such as a clinical response to a drug targeting ALDHSA1 and a haplotype ALDHSA1 gene.

Transgenic animals are also useful for studying expression of the ALDHSA1 isogenes in vivo, for in vivo screening and testing of drugs against ALDHSA1 protein and for testing the efficacy of therapeutic agents and piological system. Antibodies are useful for diagnostic and prognostic formats and therapeutic methods, for immunoprecipitating the polypeptide from solution, for detecting ALDHSA1 protein isoforms in biological samples, frozen tissue sections, for use in immunocytochemical.

Is useful for gene therapy and antisense etchniques. The polynucleotide is useful for gene therapy and antisense gene therapy. This sequence ancodes ALDHSA1 (located on chromosome 6p22), and forms a reference archain are hased described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45469 CAATACCATAAATGAATGGGTGTGGCTATGCTCTAATAACATTTTGTTTATGGACACTGA 45410
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cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immune/haematopoietic antigen genomic sequence SEQ ID NO:19625.
                                                                                                                                                                                                                                                                                                                                                                                                 3.0%; Score 69.4; DB 24; Length 46765; Similarity 57.2%; Pred. No. 8.8e-09; Conservative 0; Mismatches 121; Indels 30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein are based, described in the method of the invention.
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ID AAK64813 standard; DNA; 47319
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2000US-0180628.
2000US-0184664.
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24-FEB-2000;
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amino acid sequences given in Annabara and vaccine production. (1) arctivity, and can be used in gene therapy and vaccine production. (1) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expression in a patient's genome complement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to produce the real calcs income metastesses of haematopoietic-derived cells. AAK64703 cancers and cancer metastesses of haematopoietic antigen genomic cancers metastesses of haematopoietic antigen genomic sequences from the present invanie/max654942 to AAX854590 and AAM82169 represent sequences used in the exemplification of the present invention.

AAK54951 to AAK64702 encode the human immune/haematopoletic antigen (I)

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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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Disclosure;

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66.2%; Pred. No. 8.9e-09;
Live 0; Mismatches 51; Indels 0;
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GenCore version 4.5

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OM nucleic - nucleic search, using sw model

Run on: June 6, 2002, 08:14:48 ; Search time 2404.01 Seconds

(without alignments)

12834.406 Million cell updates/sec

Title:
Perfect score: 2286
Sequence: 1 Laatacgactcactataggg......tgacttccacggctgggacg 2286
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 200000000

Post-processing: Maximum Match 100%
Listing first 45 summaries
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## 2: em\_esthum:\* 3: em\_esthum:\* 4: em\_estn:\* 5: em\_estp:\* 6: em\_estp:\* 7: em\_estp:\* 7: em\_estp:\* 10: gb\_est:\* 10: gb\_est:\* 11: gb\_htc:\* 11: gb\_htc:\* 12: em\_gss\_hum:\* 14: em\_gss\_hum:\* 15: em\_gss\_hum:\* 16: em\_gss\_vrt:\*

em\_estba:\*

EST:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES		ID	BI262402	T58770	L44398	AQ695956	AW183569	AI125442	AQ378792	AI128823	W76494	AG154552	AI926274	AI240516	AA443938	AA44117	AI208768	BI061153	B98848
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	BI262402 mRNA Seguence. BI262402 IG.1482 Bukaryota; Metazoa; Metazoa; Mamalia; Eutheria; I (Mases I to 480) MNH-MGC http://mgc. NAtional Institutes Unpublished (1999) Contact: Robert Str Emal: capabs-remail Tissue Procurement: Preparation: Ling H Cond through the I Clond distribution Clond distribution Clond distribution High quality sequen High quality sequen High quality sequen LCAML846 I . 480 Abraefs** //db_rsefs** //db_rsefs** //db_rsefs** //db_host**
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L44398 390 bp mRNA linear EST 17-JAN-1996
HUMESTLE3 Human thymus NSTH II Homo sapiens cDNA, mRNA sequence.
L44398
L44398.1 GI:1048762
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Lamerdin, J.E., Athwal, R.S., Patanjali, S., Weissman, S. and Carrano
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/db_xref="taxon:9606"
/clone_lib="Human thymus NSTH II"
/note="From adult human thymus NSTH II cells; randomly
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llarity 62.4%; Pred. No. 9.3e-10;
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Pred. No. 8.1e-10;
0; Mismatches 35;
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Livermore, CA 94550, USA.
Location/Qualifiers
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(bases 1 to 354)

Hiller,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., Duebque,F., Eavello,A., Gish,W., Hawkins,M., Purkanba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M. Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="49 years old"
/lab_host="SolR cells (kanamycin resistant)" ite_1: EcoRI /note="Organ: liver: Vector: pBluescript SK; Site_1: EcoRI ; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               354 bp mRNA linear EST 09-FEB-1995
yb80h02.s1 Stratagene liver (#937224) Homo sapiens cDNA clone
IMAGE:77523 3', mRNA sequence.
                                                                                                                                                                                                    ö
       1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 314 286 1810
Enail: est@watson.wustl.edu
Insert Size: 2225:
High qality sequence stops: 271 Source: IMAGE Consortium, LLNL Th
clone is available royalty-free through LLNL; contact the IMAGE
Consortlum (info@image.llnl.gov) for further information.
Insert.Length.1225 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                   Score 81; DB 10; Length 480;
Pred. No. 7e-10;
0; Mismatches 35; Indels
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/sex="male"
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/db_xref="GDB:497268"
/db_xref="taxon:9606"
/clone="IMAGE:77523"
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nilarity 74.5%; 1
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/ncte="Organization" / nector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCL_CGAP_GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M. A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Unpublished (1997)
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
This cathone is available royalty-free through LLNL; contact the This chone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -400P from Gibco.
High quality sequence stop: 420.
I. cation/Qualifiers
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xj76h04.xl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:2663191 3', mRNA sequence.
AW183569
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ilarity 59.6%; Pred. No. 3.6e-09;
Conservative 0; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ImAGE:263191"
/clone=lib="Soares_NFL_T_GBC_S1"
/lab_host="DH108"
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1 (bases 1 to 521)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Halzman, T., Feller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: (206) 616-1618
Fax: (206) 616-1618
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2160 row: K column: 6
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149 CCAGAGACAATACATAAGCAAGGGGAGCTAGCTATGTTCCAATAGAACTTTATTATAAA 208
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Location/Qualifiers
1. 521
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=2160 Col=6 Row=K"
/sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Mahairas GG, Wallace JC, Hood L
Halp Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA
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                                                               209 AACAAATGGTCAACTATAGTTT 230
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Unpublished (1997)

Other GSSs: RPC111-151B24.TV

Contact: Shaying Zhao, william Nierman, Mark Adams

Contact: Shaying Zhao, william Nierman, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0208

Email: bbeetigr.org

Clones are derived from the human BAC library RPCI-11, For BAC

Library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genetics (info@resgen.com). BAC end search/pac_end_search.html:

Seq primer: SP6

Seq primer: SP6
                                                                                                                    AQ378792 658 bp DNA linear GSS 20-MAY-1999
RPCII1-151B24.TJ RPCI-11 HOMO Sapiens genomic clone RPCI-11-151B24,
                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                     1 (bases 1 to 628)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
                                                                                                                                                                                                                                                                                                                                   Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Yector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCIII Human Male BAC Library" 133 c 136 g 185 t 1 others
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   1182 tggatttggcttgtgacctacagttggccaatccctgattcccaa 1226
                      396 TTAATCTGGCCCACAAGCCATAGTTCGCCAATGCCTGTCACACA 440
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Pred. No. 4e-09;
0; Mismatches 39;
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/db_xref="GDB.7557647"
/db_xref="taxon:9606"
/clone="RRCI-11-151224"
/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Male"
/cell_type="Lymphocytes"
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Best Local Similarity 72.1%;
Matches 101; Conservative
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Mammalla; Eutherla;
                                                                                                                                                   DNA sequence.
AQ378792
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DNA Sequencing by: Washington University Genome Sequencing Center
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 592 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3
                                                                                                                                                   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 459) NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Pred. No. 3.6e-09;
0; Mismatches 113; Indels 28
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Homo sapiens

Bukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

[ (bases 1 to 411)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,

Riffin,L., Rohlifing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                           The Washurertx Est Froject Unpublished (1995)
Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Putative full length read Insert Length: 466 Std Error: 0.00
Seg primer: mob.REGA+ET.
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2d67d03.rl Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone
IMAGE:345701 5', mRNA sequence.
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Pred. No. 5.6e-09;
0; Mismatches 96;
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Best Local Similarity 60.2%;
Matches 174; Conservative (
                                                        W76494.1 GI:1386739
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 393)
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                                                                                                                                                                                                   NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                                                                                                                                                                                                         Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
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Pred. No. 5.6e-09;
0; Mismatches 96; Indels 19
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/clone_lib="Soares_fetal_heart_NbHH194"
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/organism="Homo sapiens"
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Best Local Similarity 60.28
Matches 174; Conservative
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Best Local Similarity 64.9%;
Matches 131; Conservative (
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
L-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 330-0045, Japan
(E-mail: chimpbeségsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
end was generated during the R&D process and may have higher chance
                                                                                                                    4552 680 bp DNA linear GSS 09-JAN-2002 troglodytes DNA, clone: RP43-018J16.TJ, genomic survey
                                                                                                                                                                                 AGIS4552.1 GI:16684230
GSS: GSS (genome survey sequence).
Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee
Male BAC_Library clone:RP43-018J16.TJ.
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                                                                                                                                                                                                                                                  Pan troglodytes'
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                941 ttttaggetetgtgtgecatatggteteagteacaactacteatetetgeetetgtagea 1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
127 c 133 g 213 t
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3.4%; Score 77.4; DB 12; Length 680;
Best Local Similarity 62.6%; Pred. No. 6.5e-09;
Matches 137; Conservative 0; Mismatches 81; Indels 1
1122 aacgtaaaaactactcttaggtcgcaaggttaaggccattctcagcttag 1170
                   -ttatggatacggaaacctgaaaataatgtctttctttt 1098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. 680
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-018J16.TJ"
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R.Site 1 : EcoRI
R.Site 2 : EcoRI.
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Tunor Gene Index
Institute, Cancer Genome Anatomy Project (CGAP),
Tunor Gene Index
In Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Email: buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Seq primer: -40UP from Gibco
High quality sequence stop: 382.
A1926274 400 bp mRNA linear EST 02-SEP-1999 W043906.xl NCI_CGAP_Gas4 Homo sapiens CDNA clone IMAGE:2458138 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST 30-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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/tissuc_type="poorly differentiated adenocarcinoma with
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Pred. No. 6.3e-09;
0; Mismatches 68; Indels 3
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/sex="maile" /sex="maile" /lab_host="Dispersors" /sex="maile" /lab_host="DH10B" /lab
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 393)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
                                                                                                                                                                        Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1800
Email: est@watson.wustl.edu
This clone is available royalty-free through LLML; contact the
IMAGE Consortium (info@lange.llnl.gov) for further information.
Seq primer: -4.lml3 fwd. ET from Amersham
High quality sequence stop: 321.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .386
/organism="Homo sapiens"
/db_xref="CDB:5977767"
/db_xref="taxon:9606"
/clone="IMAGE:757156"
/clone=lib="Soares_testis_NHT"
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Matches 119; Conservative
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AA44117/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / note-"Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NDHL19W, testis NHT, and B-cell NCI_CGAP_CGBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.W.A.G.E. clones 297480-302087, 682632-667239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA443938 386 bp mRNA linear EST 03-JUN-1997 zv51c03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757156 aA443938
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I Chases I to 32. No. 25. http://www.ncbi.nlm.nih.gov/ncicgap. Nor-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. Natlonal Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 386)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs.remail.nih.gov

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (lift@image.llnl.gov) for further information.

Insert Length: 735 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 315.

Location/Qualifiers
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                           AI240516
AI240516,1 GI:3835913
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Unpublished (1997)
                                                                                                                                             Homo sapiens
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WashU-Merck EST Project 1997
Unpublished (1997)
Contact: Wilson RK
WashIngton University School of Medicine
4444 Forest Park Parkay, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                              Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
Seq primer: -28ml3 rev2 ET from Amersham
Location/Oualifiers
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1.019anism="Homo sapiens"
Ab_xref="GDB:5977767"
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Ab_xref="Laxon:5806"
Allone="ImAGE:757156"
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution. NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Insert Length: 605 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 412.
Location/Qualifiers
                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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63.0%; Pred. No. 7.2e-09;
Live 0; Mismatches 70; Indels
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/clone_lib="Soares_testis_NHT"
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Job time: 8926 sec
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                    Tumor Gene Index
Unpublished (1997)
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INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-917-894-210

US-08-925-028-42

US-08-925-028-42

US-08-925-108-91

US-09-124-698-91

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
US-09-200-284-2
US-08-967-101-48
US-08-124-698-48
US-09-124-698-48
US-09-124-698-48
US-09-124-698-48
US-09-124-698-48
US-09-133-817-3
US-09-007-005-17
US-09-313-300-6
US-09-138-155-17
US-09-128-155-17
US-09-138-155-17
US-09-138-155-17
US-09-138-155-17
US-09-138-155-17
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Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: SCHEIFLINGER, F. APPLICANT: SCHEIFLINGER, F. APPLICANT: FALMER, F. G. TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-797-906-3
US-09-128-155-16
US-08-742-185-101
US-08-480-346-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATYONEN AGGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
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ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
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COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDLE
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,789A
                                                                                                                                                                                                                                                                                                                                                                                                         ; DB 4;
1.9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 292
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed IP Law Group
STREET: 701 Fifth Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                        Score 67.6; DE
Pred, No. 1.9e-
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
21P: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
                                                                      US-09-305-384-1; Sequence 1, Application US/09305384; Patent No. 6242218; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith, John M.
Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                         3.0%;
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STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
COCGANISM: Homo sapiens
US-09-305-384-1
                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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US-08-991-789A-210
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Patent No. 644218
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Treco, Douglas A.
APPLICANT: Heartlein, Michael W.
APPLICANT: Selden, Richael W.
APPLICANT: Selden, Richael W.
TITLE OF INVENTION: GENOMIC SEQUENCES FOR PROTEIN PRODUCTION AND DELIVERY
FILE REPERENCE: 07236/017001
CURRENT FILING DATE: 1999-05-05
EARLIER APPLICATION NUMBER: US 60/084,649
EARLIER APPLICATION NUMBER: US 60/084,649
EARLIER PILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cettecteagacagagtgagetacteacgateceaggtgtaceetgaggecagecaaggt 278
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                                                              159 agotoatoggaggotgaggoccaggcacatgtttgcctgaactatccatgttatatgatt 218
                                  Gaps
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 Length 7218;
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Pred. No. 1.8e-10;
0: Mismatches 74;
    Score 71.8; DB 1;
Pred. No. 9.7e-12;
37; Mismatches 144;
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                                16; Conservative 237;
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illarity 63.7%;
Conservative (
                 4.08;
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Best Local Similarity
Matches 135; Conserv
      Query Match
Best Local Similarity
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US-09-305-384-5
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                                  Matches
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APPLICANT: Treco, Douglas A.
APPLICANT: Treco, Douglas A.
APPLICANT: Heartlein, Michael W.
APPLICANT: Selden, Richard F
TITLE OF INVENTION: GROWIC SEQUENCES FOR PROTEIN PRODUCTION AND DELIVERY
FILE REFERENCE: 07236/017001
CURRENT APPLICATION NUMBER: US/09/305,384
CURRENT APPLICATION NUMBER: US 60/084,649
EARLIER APPLICATION NUMBER: US 60/084,649
EARLIER FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 6679
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                                                                                                                                                                                                                                                                                                                                                                                                    Length 6679;
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Gaps

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891 ctggacccaggttgggcaaactcttcctgtaaagaaccagacaggaactattttaggctc 950
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                                         Score 62.2; DB 4; Length 178;
Pred. No. 9.6e-10;
0; Mismatches 33; Indels
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Best Local Similarity 9.0%; Pred. No. 9.4e-06;
Matches 28; Conservative 162; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
WUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
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CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, STEPPEN A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                         2.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 7218 base pairs
TYPE: nucleic acid
                                                              Best Local Similarity 71.3
Matches 82; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                             Query Match
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Patent No. 6344550
Patent No. 6344550
APPLICANT: Frudakis, Tony N. APPLICANT: Smith, John M. APPLICANT: Reed, Steven G. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER NUMBER OF SEQUENCES: 297
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                             Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                    33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/062,451 FILING DATE: US/09/062,451 CLASSIFICATION:
              ATTORNEY/AGENT INPORMATION:

NAME: POTTER, Jane E. R.
REGISTRATION NUMBER: 33,332
REPERBECEDOCKET NUMBER: 210121.419C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELERA: (206) 682-6031
INFORMATION FOR SEQ ID NO: 210:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                           Score 62.2; DB 4;
Pred. No. 9.6e-10;
0; Mismatches 33;
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; SEQUENCE DESCRIPTION: SEQ ID NO: 210:
US-08-991-789A-210
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
FILING DATE: 11-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.7%;
Best Local Similarity 71.3%;
Matches 82; Conservative
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TELEFAX: (206) 682-6031
INFORMATION FOR SEO ID NO: 210
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : LENGTH: 178 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
US-09-062-451-210
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ZIP: 98104-7092
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US-09-062-451-210
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Patent No. 6306402
GENERAL INFORMATION:
APPLICANT: Read, Steven G.
APPLICANT: Houghton, Raymond
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lodes, Michael J.
APPLICANT: Hodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: MCNOtill, Particla D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF EHRLICHIA INFECTION
FILE REFERENCE: 20121.439C4
CURRENT APPLICATION NUMBER: US/09/295,028
CURRENT FILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 85
SOFTWARE: FastSEQ for Windows Version 3.0
SED ID NO 42
FEMBLE OF AUGUST AND AUGUST AND AUGUST AUG
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Pred. No. 9.7e-06;
0; Mismatches 40; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,582
FILING DATE: 29-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Washington
                                                                                                                                                                                                                                                                               Sequence 42, Application US/09295028 Patent No. 6277381
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67.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.3
Best Local Similarity 67.2
Matches 90; Conservative
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                                                                                                                                        3416 GATGAGCATGACTC 3429
                                                                                    1030 aacatatgtgaccc 1043
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Ehrlichia sp.
US-09-295-028-42
                                                                                                                                                                                                                                RESULT 8
US-09-295-028-42
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                                                    ttcctgtaaagaaccagacaggaactattttaggctctgtgtgccatatggtc----tca 969
                                                                                                                                                                                                                                atagecaageagaetgetggecagggattgeaaaggagtatttgtttgettaagaaaat 723
     ctaaatccacatggtgggaaggggggagtggggaagagagtgcgctgtggggctgtgcc 603
                                                                                                                       tacttctggagggtaagactcggggccctccaggaacaaaggattcaggctggtggcagct 663
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Patent No. 6207169
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Hodds, Michael J.
APPLICANT: Houghton, Raymond
TILLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 3786;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 1997
CLASSIFICATION: 424
ATTONEY/AGENT INPORMATION:
NAME: MAKI, DAVIG J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.439
TELECOMMULCATION INFORMATION:
TELECOMMULCATION:
TELECOMMULCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SEQUENCE CHARACTERISTICS:
LENGTH: 3786 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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ilarity 67.2%;
Conservative
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COUNTRY: USA
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US-08-975-762-42
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Best Local Simi
Matches 90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3786;
                                                                                                                                                                                                                                                                                                                     40; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
FILING DATE: 10.NOV-1997
                                                                                                                                                                                                                                                                                     Query Match 2.3%; Score 52; DB 4; 1
Best Local Similarity 67.2%; Pred. No. 9.7e-06;
Matches 90; Conservative 0; Mismatches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CLASSIFICATION:
ATTORNEY-AGBNT INFORMATION:
NAME: MAKI, DAVIG J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 10-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEPAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
                                                             REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
                                                                                                                        INFORMATION FOR SEQ ID NO: 42: SEQUENCE CHARACTERISTICS: LENGTH: 3786 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-106-582-42
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                                                                                                                                                                                                                                                                                                                                                                             322 ACACTCAACTGTACTGTAAAGGTGAAAGCAGGCACAGACAATGTATTAACCAAGGAGG 381
                                                                                                                                                                 Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 91, Application US/08592541
Patent No. 5986054
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.2%; Score 50.6; DB 2; Length 502; Best Local Similarity 64.3%; Pred. No. 7.6e-06; Matches 92; Conservative 0; Mismatches 49; Indels
                                                                                                                                                                                                         49; Indels
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SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/For C
                                                                                                                                                            Query Match 2.2%; Score 50.6; DB 2; Best Local Similarity 64.3%; Pred. No. 7.6e-06; Matches 92; Conservative 0; Mismatches 49;
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High Street Tower - 125 High Street
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MEDIUM TYPE:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
; TYPE: nucleic acid
; STRANDENNES: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-967-101-91
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MOLECULE TYPE: DNA (genomic)
US-08-592-541-91
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TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 502 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Massachusetts
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                                                          GENERAL INFORMATION:
APPLICANT: ST. GENGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: RASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
CORRESPONDENCES: 183
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.2%; Score 50.6; DB 4; Length 56 Best Local Similarity 64.3%; Pred. No. 7.6e-06; Matches 92; Conservative 0; Mismatches 49; Indels
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                                                                                                                                                                                                                                              TESTA, HURWITZ & THIBEAULT
gh Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
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; Sequence 91, Application US/08496841C
Partent No. 6210919
; GENERAL INFORMATION:
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ROMMENS, JOHANNA M
FRASER, PAUL E
                  Sequence 91, Application US/09127480 Patent No. 6194153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Pitcher, Edmund R.
TPLECOMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
TELEPAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 502 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 502 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-127-480-91
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                    ADDRESSEE: TESTA, ....
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                                                                                                                                                                                                                                                                                                                STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                     U.S.A.
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                                                                                                                                                                                                                                                                                        Boston
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                                                                                                                                                                                                                                                                                                                                                        02110
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US-09-127-480-91
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                977 ctactcatctctgcctctgtagcacgaaagcaattagcaacaatatgtcaacaaaaatat 1036
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                                                                                                                                                                                                                                                                                                                              APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROWMENS, JOHANNA M
APPLICANT: ROMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
CORRESPONDENCE SI 183
CORRESPONDENCE ADDRESS:
ADDRESSE: TESTA, HURMITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.2%; Score 50.6; DB 3; Length 502; 64.3%; Pred. No. 7.6e-06; tive 0; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,698 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                          1037 gtgaccccatgaaaactttattt 1059
                                                                                                                                                                                                                                                                 Sequence 91, Application US/09124698
Patent No. 6117978
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic) US-09-124-698-91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 502 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 64.39
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Boston
STATE: Massachusetts
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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Length 502;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL ST. GENGE-HYSLOP, PETER H
APPLICANT: ST. GENGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: BOSLON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.2%; Score 50.6; DB 4; Length 502; Best Local Similarity 64.3%; Pred. No. 7.6e-06; Matches 92; Conservative 0; Mismatches 49; Indels
                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/08/496,841C
ALLING DATE: 28-Jun-1995
CLASSIFICATION: <UNKNOWID>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 91:
US-08-496-841C-91
                                                                                                                                                                                                                                                                                                                                         ATTORREY/AGERT INFORMATION:
NAME: Paul F. Fehlner, Ph.D.
REGISTRATION NUMBER: 35,135
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEPHONE: (212) 753-6237
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
ADDRESSEE: Darby & Darby,
STREET: 805 Third Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/08967101 Patent No. 5840540
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                                                                                                                                                                MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 502 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                 STATE: New York COUNTRY: U.S.A. ZIP: 10022 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Massachusetts: U.S.A.
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